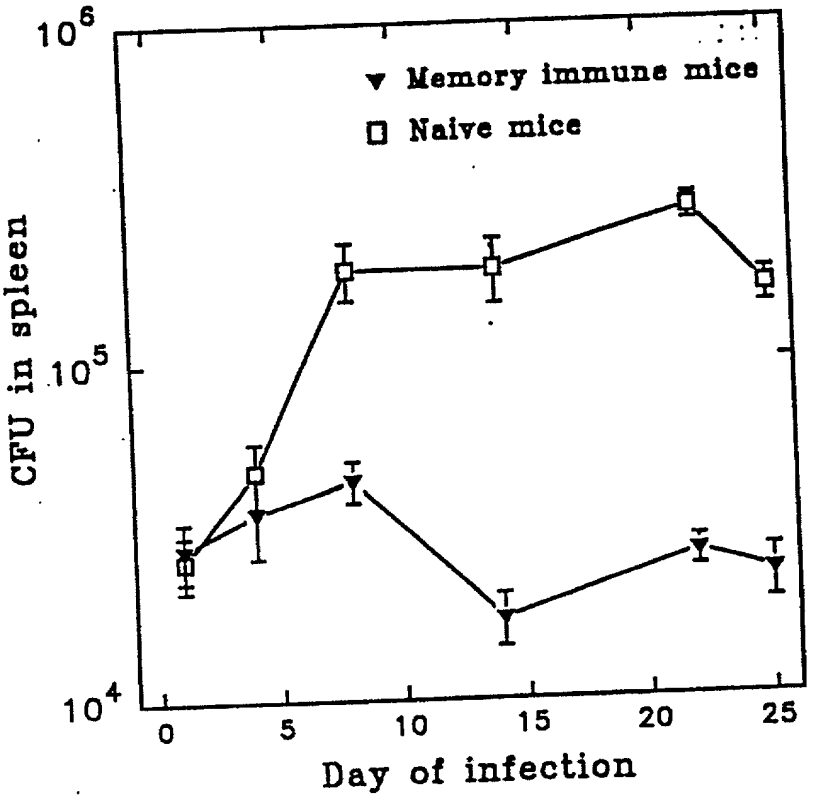

10^6
10^5
10^4
CFU in spleen
Memory immune mice
Naive mice
0
5
10
15
20
25
Day of infection

Fig. 1

Fig. 1

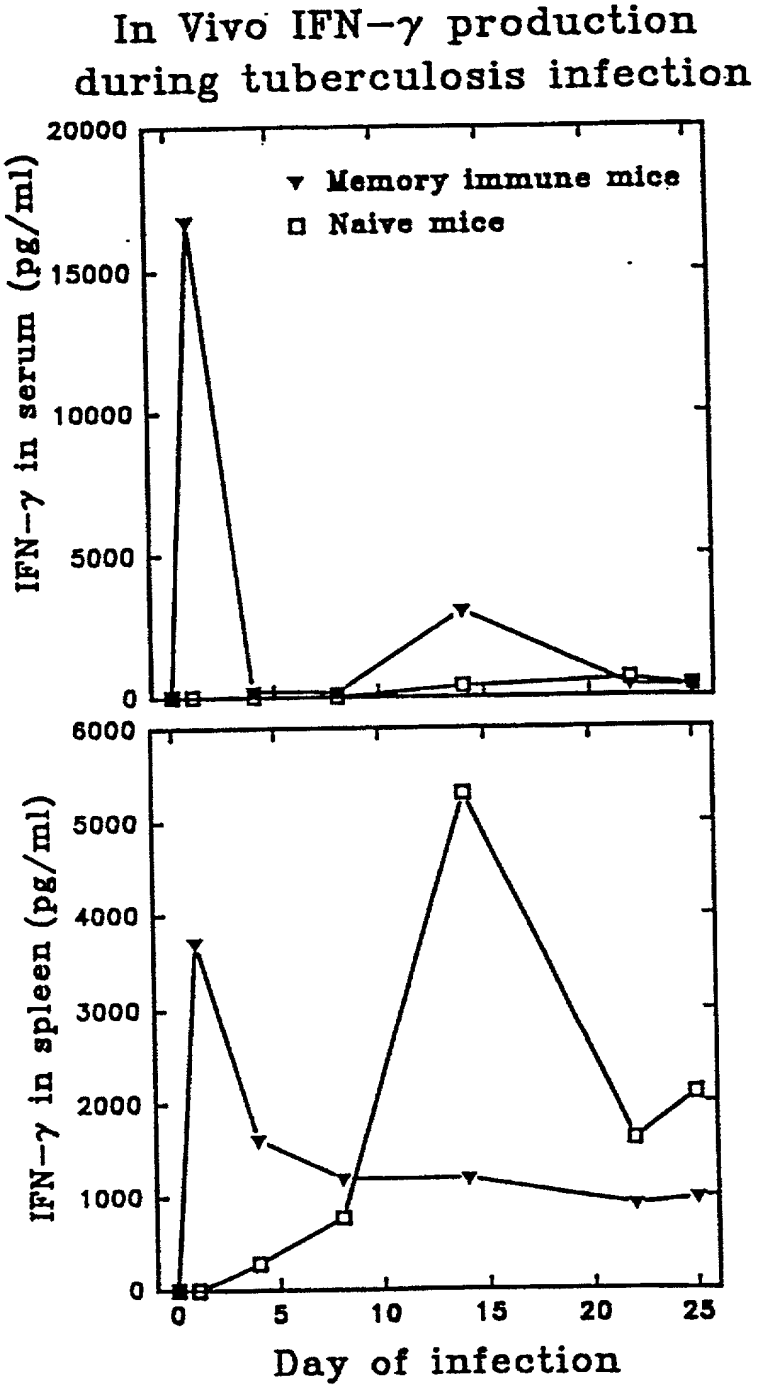

In Vivo IFN−γ production
during tuberculosis infection
Memory immune mice
Naive mice
IFN−γ in serum (pg/ml)
20000
15000
10000
5000
0
IFN−γ in spleen (pg/ml)
6000
5000
4000
3000
2000
1000
0
0
5
10
15
20
25
Day of infection

Fig. 2

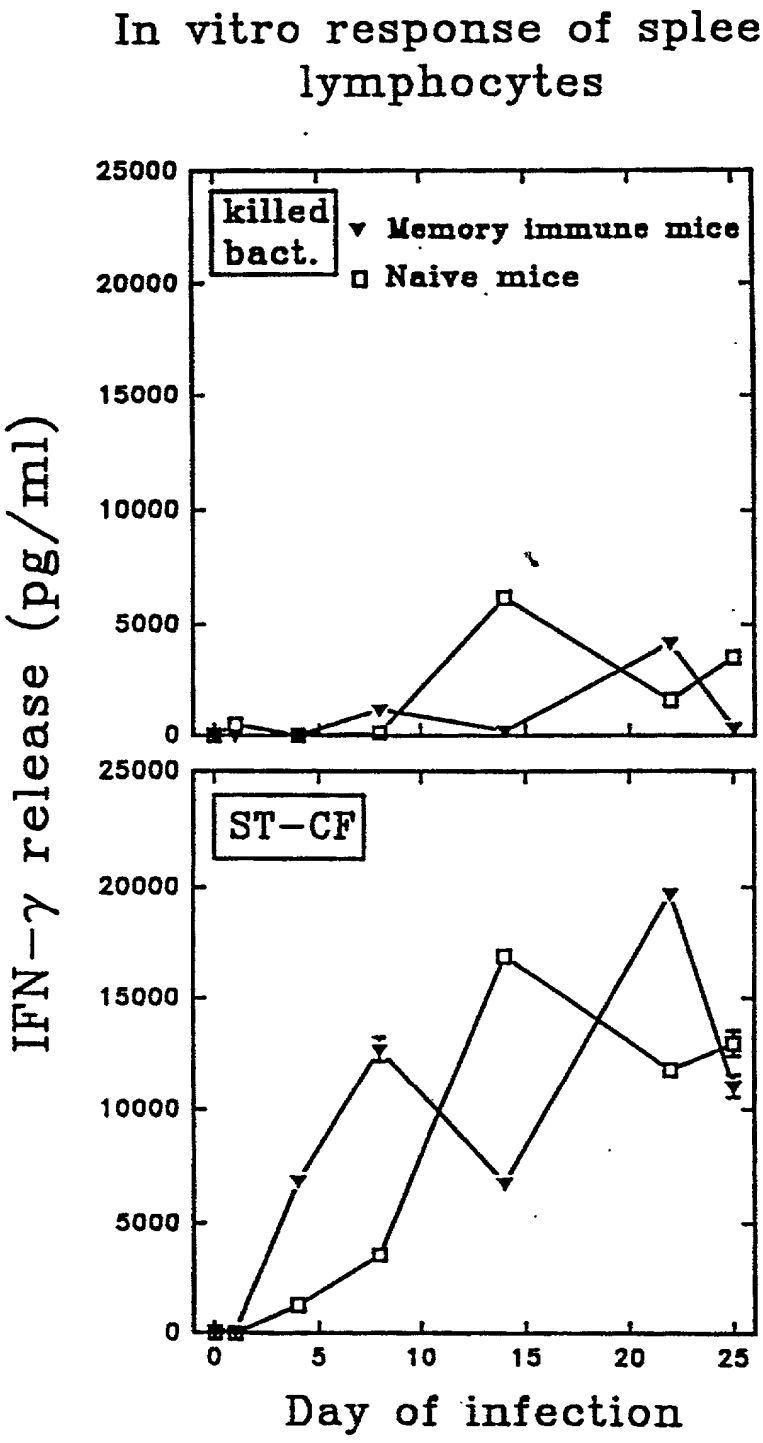

In vitro response of spleen lymphocytes
killed bact.
Memory immune mice
Naive mice
ST-CF
IFN-γ release (pg/ml)
Day of infection
25000
20000
15000
10000
5000
0
0
5
10
15
20
25

Fig. 3

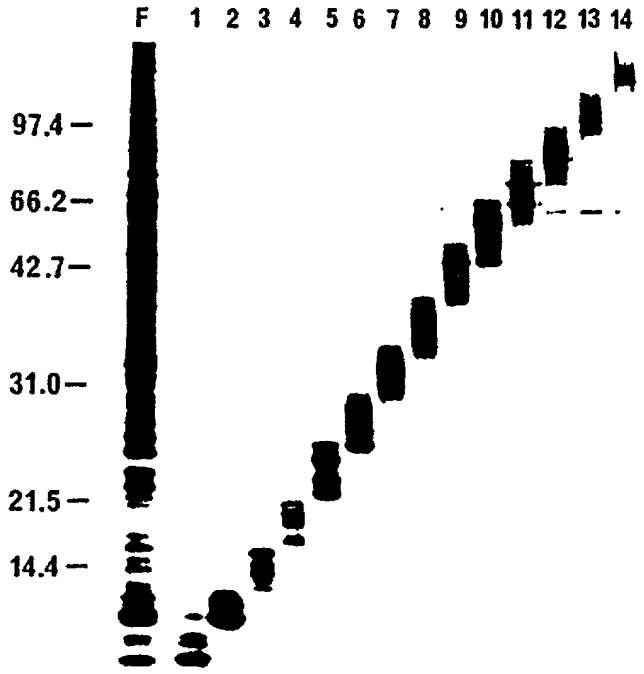


Fig. 4

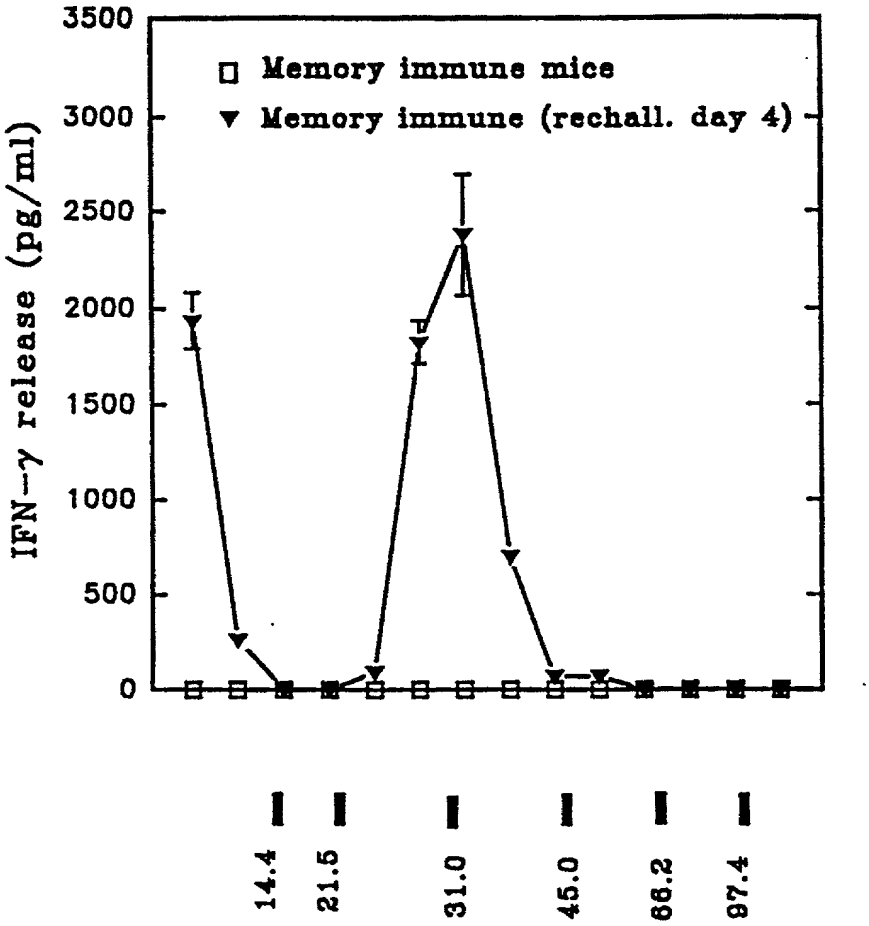

3500
3000
2500
2000
1500
1000
500
0
IFN-γ release (pg/ml)
Memory immune mice
Memory immune (rechall. day 4)
14.4
21.5
31.0
45.0
66.2
97.4

Fig. 5

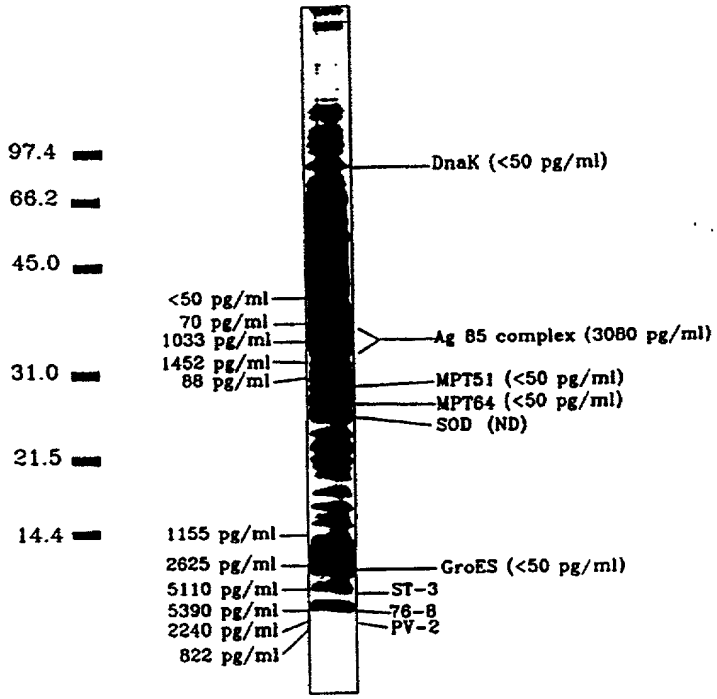
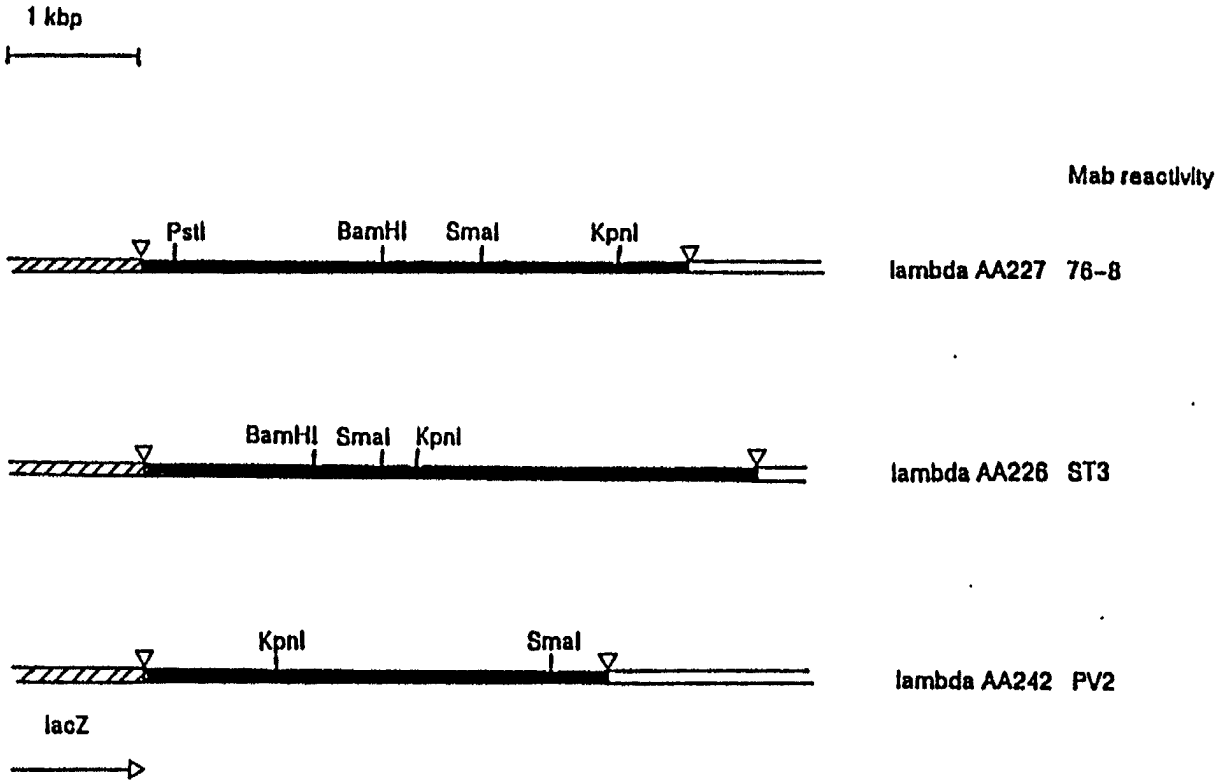

97.4
66.2
45.0
31.0
21.5
14.4
DnaK (<50 pg/ml)
<50 pg/ml
70 pg/ml
1033 pg/ml
1452 pg/ml
88 pg/ml
Ag 85 complex (3080 pg/ml)
MPT51 (<50 pg/ml)
MPT64 (<50 pg/ml)
SOD (ND)
1155 pg/ml
2625 pg/ml
5110 pg/ml
5390 pg/ml
2240 pg/ml
822 pg/ml
GroES (<50 pg/ml)
ST-3
76-8
PV-2

Fig. 6



Physical map of recombinant lambda phages expressing products reactive with Mabs recognizing low M.W. components

Fig. 7

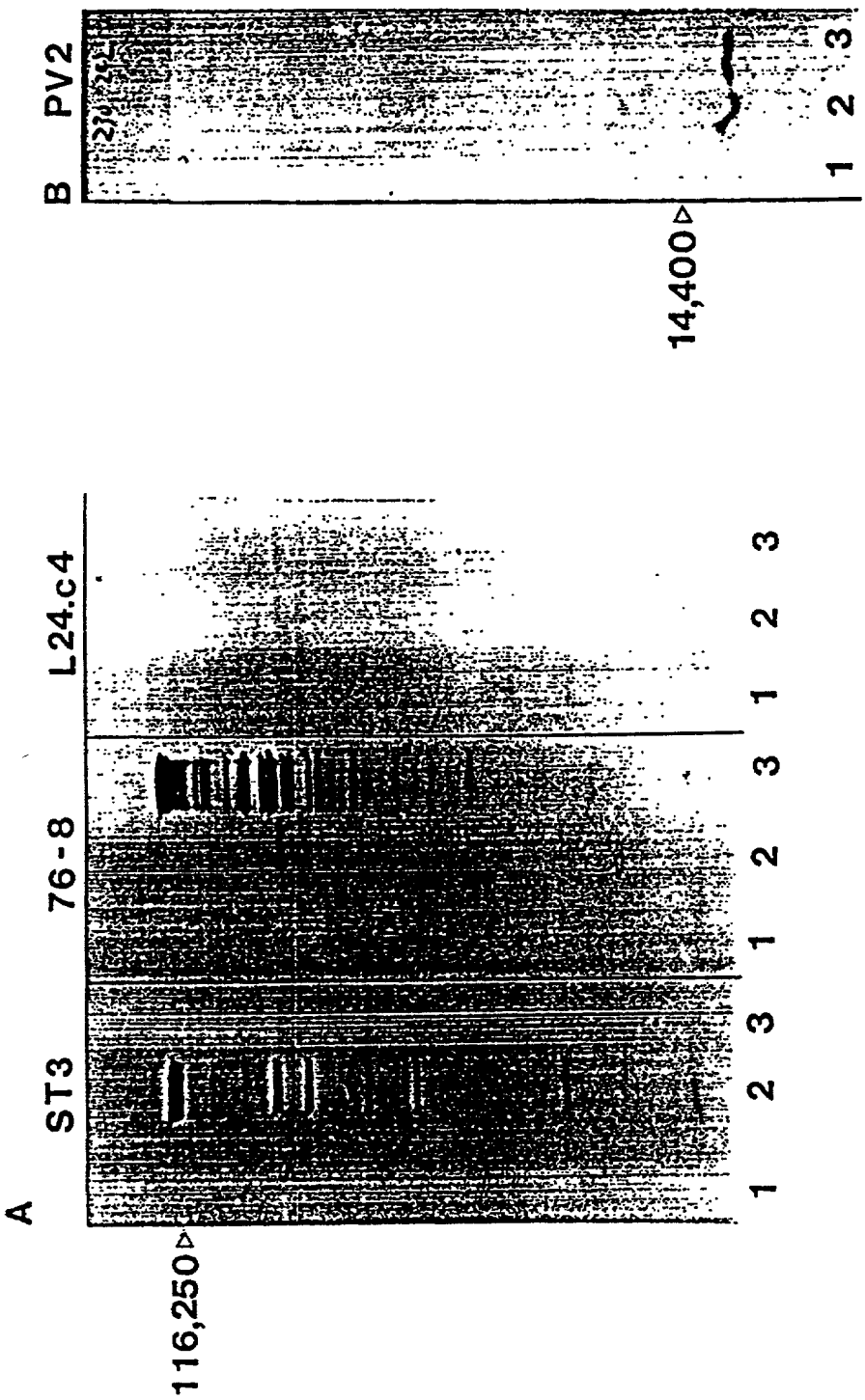


Fig. 8

```
  1  GGCCGCCGGT ACCTATGTGG CCGCCGATGC TGCGGNCGCG TCGACCTATA CCGGGTTCTG                         60
                -35region                           -10 region
 61  ATCGAACCCT GCTGACCGAG AGGACTTGTG   ATG TCG CAA ATC ATG TAC AAC TAC CCC GCG               120
                    Shine Delgarno       M   S   Q   I   M   Y   N   Y   P   A
121  ATG TTG GGT CAC GCC GGG GAT ATG GCC GGA TAT GCC GGC ACG CTG CAG AGC TTG GGT GCC          180
      M   L   G   H   A   G   D   M   A   G   Y   A   G   T   L   Q   S   L   G   A
181  GAG ATC GCC GTG GAG CAG GCC GCG TTG CAG AGT GCG TGG CAG GGC GAT ACC GGG ATC ACG          240
      E   I   A   V   E   Q   A   A   L   Q   S   A   W   Q   G   D   T   G   I   T
241  TAT CAG GCG TGG CAG GCA CAG TGG AAC CAG GCC ATG GAA GAT TTG GTG CGG GCC TAT CAT          300
      Y   Q   A   W   Q   A   Q   W   N   Q   A   M   E   D   L   V   R   A   Y   H
301  GCG ATG TCC AGC ACC CAT GAA GCC AAC ACC ATG GCG ATG ATG GCC CGC GAC ACC GCC GAA          360
      A   M   S   S   T   H   E   A   N   T   M   A   M   M   A   R   D   T   A   E
361  GCC GCC AAA TGG GGC GGC TAG                                                               381
      A   A   K   W   G   G   •
```

Fig. 9

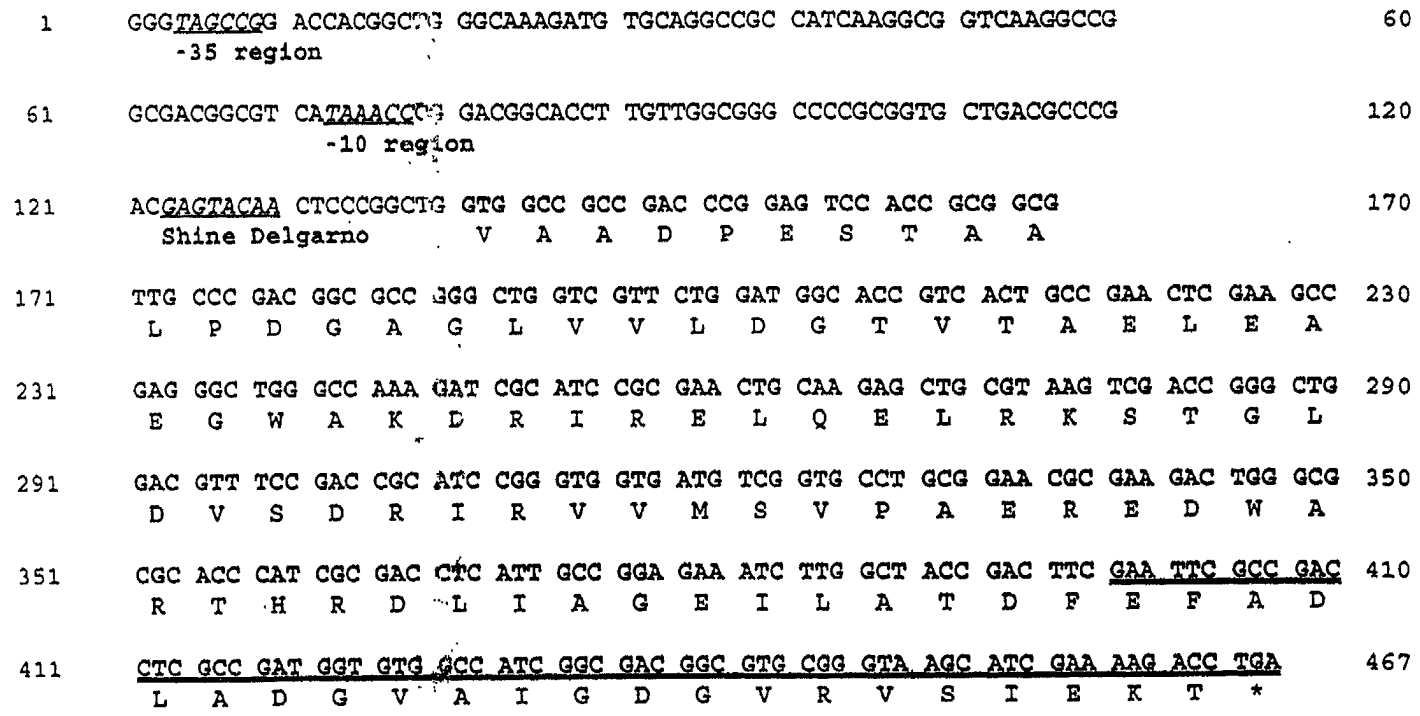

1 GGGTAGCCGG ACCACGGCTG GGCAAAGATG TGCAGGCCGC CATCAAGGCG GTCAAGGCCG 60
-35 region
61 GCGACGGCGT CATAAACCTG GACGGCACCT TGTTGGCGGG CCCCGCGGTG CTGACGCCCG 120
-10 region
121 ACGAGTACAA CTCCCGGCTG GTG GCC GCC GAC CCG GAG TCC ACC GCG GCG 170
Shine Delgarno V A A D P E S T A A
171 TTG CCC GAC GGC GCC GGG CTG GTC GTT CTG GAT GGC ACC GTC ACT GCC GAA CTC GAA GCC 230
L P D G A G L V V L D G T V T A E L E A
231 GAG GGC TGG GCC AAA GAT CGC ATC CGC GAA CTG CAA GAG CTG CGT AAG TCG ACC GGG CTG 290
E G W A K D R I R E L Q E L R K S T G L
291 GAC GTT TCC GAC CGC ATC CGG GTG GTG ATG TCG GTG CCT GCG GAA CGC GAA GAC TGG GCG 350
D V S D R I R V V M S V P A E R E D W A
351 CGC ACC CAT CGC GAC CTC ATT GCC GGA GAA ATC TTG GCT ACC GAC TTC GAA TTC GCC GAC 410
R T H R D L I A G E I L A T D F E F A D
411 CTC GCC GAT GGT GTG GCC ATC GGC GAC GGC GTG CGG GTA AGC ATC GAA AAG ACC TGA 467
L A D G V A I G D G V R V S I E K T *

Fig. 10

1 *GAATT*CGCCGGGTGCACACAGCCTTACACGACGGAGGTGGACACATGAAG 50
M K
51 GGTCGGTCGGCGCTGCTGCGGGCGCTCTGGATTGCCGCACTGTCATTCGG 100
G R S A L L R A L W I A A L S F G
101 GTTGGGCGGTGTCGCGGTAGCCGCGGAACCCACCGCCAAGGCCGCCCCAT 150
L G G V A V A A E P T A K A A P
151 ACGAGAACCTGATGGTGCCGTCGCCCTCGATGGGCCGGGACATCCCGGTG 200
Y E N L M V P S P S M G R D I P V
201 GCCTTCCTAGCCGGTGGGCCGCACGCGGTGTATCTGCTGGACGCCTTCAA 250
A F L A G G P H A V Y L L D A F N
251 CGCCGGCCCGGATGTCAGTAACTGGGTCACCGCGGGTAACGCGATGAACA 300
A G P D V S N W V T A G N A M N
301 CGTTGGCGGGCAAGGGGATTTCGGTGGTGGCACCGGCCGGTGGTGCGTAC 350
T L A G K G I S V V A P A G G A Y
351 AGCATGTACACCAACTGGGAGCAGGATGGCAGCAAGCAGTGGGACACCTT 400
S M Y T N W E Q D G S K Q W D T F
401 CTTGTCCGCTGAGCTGCCCGACTGGCTGGCCGCTAACCGGGGCTTGGCCC 450
L S A E L P D W L A A N R G L A
451 CCGGTGGCCATGCGGCCGTTGGCGCCGCTCAGGGCGGTTACGGGGCGATG 500
P G G H A A V G A A Q G G Y G A M
501 GCGCTGGCGGCCTTCCACCCCGACCGCTTCGGCTTCGCTGGCTCGATGTC 550
A L A A F H P D R F G F A G S M S
551 GGGCTTTTTGTACCCGTCGAACACCACCACCAACGGTGCGATCGCGGCGG 600
G F L Y P S N T T T N G A I A A
601 GCATGCAGCAATTCGGCGGTGTGGACACCAACGGAATGTGGGGAGCACCA 650
G M Q Q F G G V D T N G M W G A P
651 CAGCTGGGTCGGTGGAAGTGGCACGACCCGTGGGTGCATGCCAGCCTGCT 700
Q L G R W K W H D P W V H A S L L
701 GGCGCAAAACAACACCCGGGTGTGGGTGTGGAGCCCGACCAACCCGGAG 750
A Q N N E R V W V W S P T N P G
751 CCAGCGATCCCGCCGCCATGATCGGCCAAACCGCCGAGGCGATGGGTAAC 800
A S D P A A M I G Q *T* A E A M G N
801 AGCCGCATGTTCTACAACCAGTATCGCAGCGTCGGCGGGCACAACGGACA 850
S R M F Y N Q Y R S V G G H N G H
851 CTTCGACTTCCCAGCCAGCGGTGACAACGGCTGGGGCTCGTGGGCGCCCC 900
F D F P A S G D N G W G S W A P
901 AGCTGGGCGCTATGTCGGGCGATATCGTCGGTGCGATCCGCTAAGC*GAAT* 950
Q L G A M S G D I V G A I R .
951 *TC* 952

Fig. 11

2-DE reference map of ST-CF

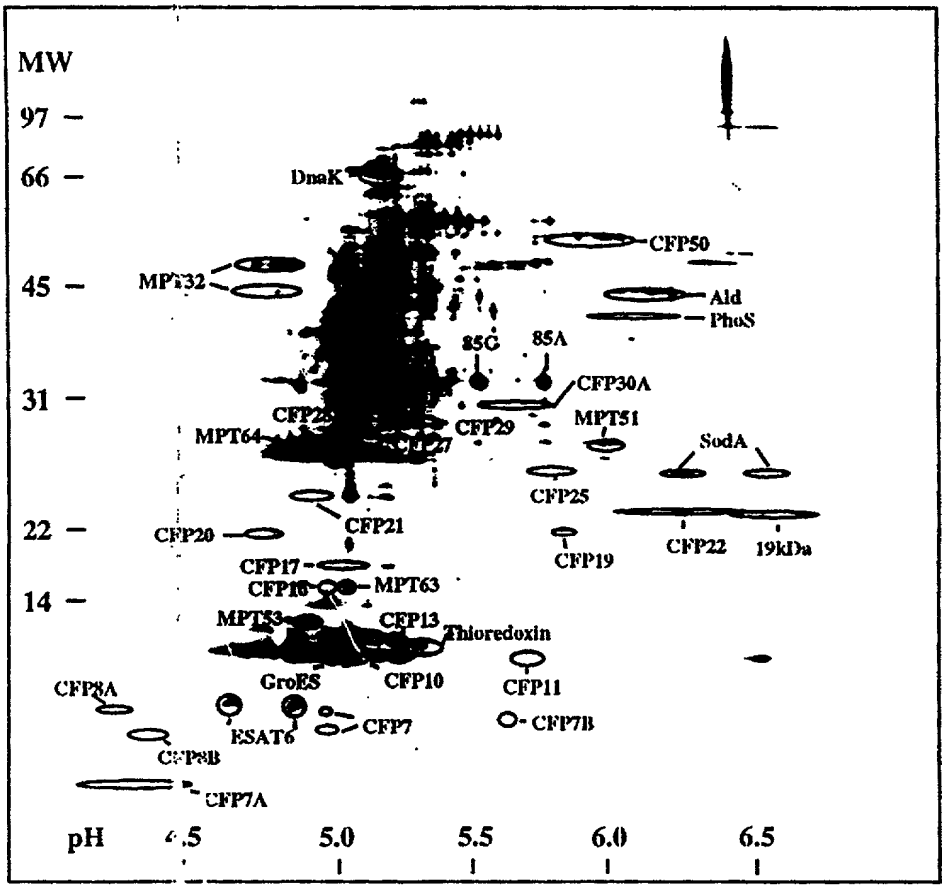
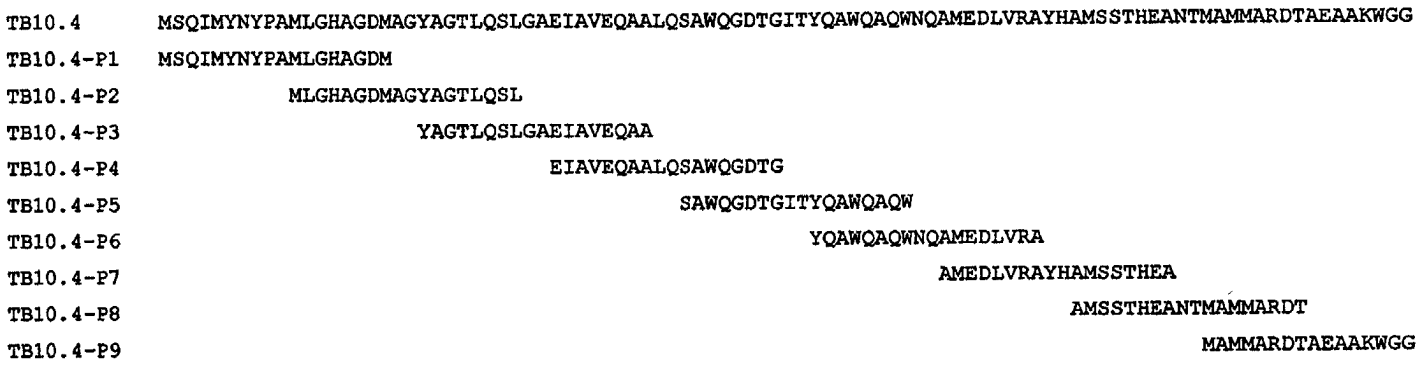


Fig. 12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TB10.4-P1 MSQIMYNYPAMLGHAGDM
TB10.4-P2 MLGHAGDMAGYAGTLQSL
TB10.4-P3 YAGTLQSLGAEIAVEQAA
TB10.4-P4 EIAVEQAALQSAWQGDTG
TB10.4-P5 SAWQGDTGITYQAWQAQW
TB10.4-P6 YQAWQAQWNQAMEDLVRA
TB10.4-P7 AMEDLVRAYHAMSSTHEA
TB10.4-P8 AMSSTHEANTMAMMARDT
TB10.4-P9 MAMMARDTAEAAKWGG

Fig. 13

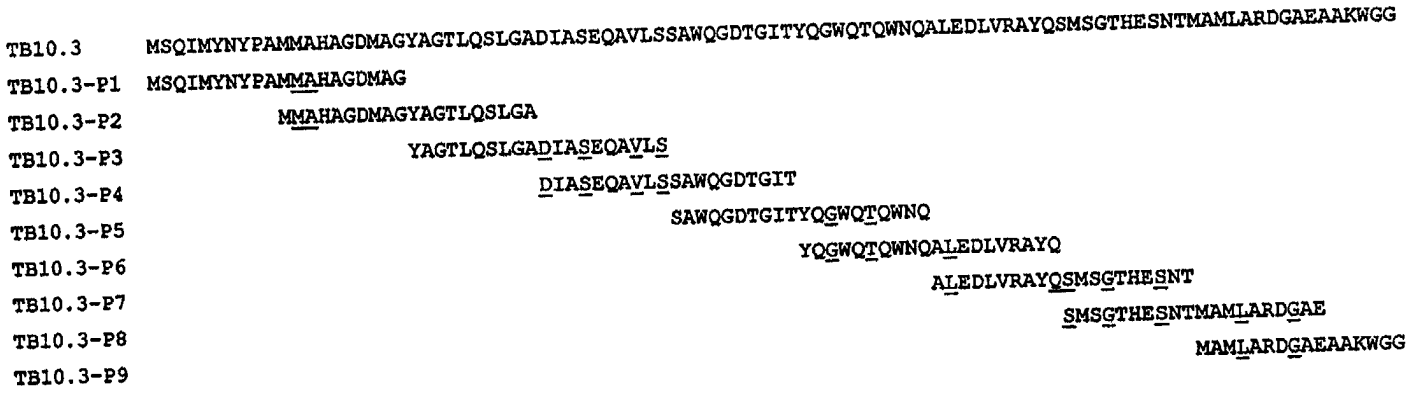
TB10.3 MSQIMYNYPAMMAHAGDMAGYAGTLQSLGADIASEQAVLSSAWQGDTGITYQGWQTQWNQALEDLVRAYQSMSGTHESNTMAMLARDGAEAAKWGG
TB10.3-P1 MSQIMYNYPAMMAHAGDMAG
TB10.3-P2 MMAHAGDMAGYAGTLQSLGA
TB10.3-P3 YAGTLQSLGADIASEQAVLS
TB10.3-P4 DIASEQAVLSSAWQGDTGIT
TB10.3-P5 SAWQGDTGITYQGWQTQWNQ
TB10.3-P6 YQGWQTQWNQALEDLVRAYQ
TB10.3-P7 ALEDLVRAYQSMSGTHESNT
TB10.3-P8 SMSGTHESNTMAMLARDGAE
TB10.3-P9 MAMLARDGAEAAKWGG

Fig. 14

TB12.9	MSQSMYSYPAMTANVGDMAGYTGTTQSLGADIASERTAPSRACQGDLGMSHQDWQAQWNQAMEALARAYRRCRRALRQIGVLERPVGDSSDCGTIRVGSFRGRWLDPRHAGPATAADAGD
TB12.9-P1	MSQSMYSYPAMTANVGDMAG
TB12.9-P2	MTANVGDMAGYTGTTQSLGA
TB12.9-P3	YTGTTQSLGADIASERTAPS
TB12.9-P4	DIASERTAPSRACQGDLGMS
TB12.9-P5	RACQGDLGMSHQDWQAQWNQ
TB12.9-P6	HQDWQAQWNQAMEALARAYR
TB12.9-P7	AMEALARAYRRCRRALRQIG
TB12.9-P8	RCRRALRQIGVLERPVGDSS
TB12.9-P9	VLERPVGDSSDCGTIRVGSF
TB12.9-P10	DCGTIRVGSFRGRWLDPRHA
TB12.9-P11	RGRWLDPRHAGPATAADAGD

Fig. 15